

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 11, 2002, 14:47:39 ; Search time 1478.06 Seconds
(without alignments)
17934.333 Million cell updates/sec

Title: US-09-911-513-1

Perfect score: 1964

Sequence: 1 taataatcattttttttt.....tctaaattactcacactggc 1964

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674877542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_esti:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_gss:*
- 13: em_gss_hum:*
- 14: em_gss_inv:*
- 15: em_gss_pln:*
- 16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------------|---------------------|
| 1 | 362.6 | 18.5 | 626 | 9 BE204113 | BE204113. EST396789 |
| 2 | 360 | 18.3 | 376 | 10 BE525349 | BE525349 M7A6STM A |
| 3 | 342.6 | 17.4 | 563 | 10 BI270025 | BI270025 NF003D04F |
| C | 333.4 | 17.0 | 372 | 10 Z34599 | Z34599 ATTS3359 Ve |
| 5 | 333.4 | 17.0 | 457 | 10 T22782 | T22782 4790 Lambda |
| 6 | 306.4 | 15.6 | 1064 | 9 BE035220 | BE035220 MO01E08 M |
| 7 | 302.2 | 15.4 | 743 | 9 AW774515 | AW774515 EST333666 |
| 8 | 298 | 15.2 | 343 | 10 Z34183 | Z34183 ATTS3217 Ve |
| 9 | 291.4 | 14.8 | 579 | 9 AW704479 | AW704479 sk53612.y |
| 10 | 286.8 | 14.6 | 579 | 10 BI498716 | BI498716 saizifil. |
| C | 283 | 14.4 | 739 | 12 BH552965 | BH552965 BOHUA01TR |
| 12 | 281.4 | 14.3 | 549 | 10 BM177886 | BM177886 saj6f05. |
| 13 | 281.2 | 14.3 | 543 | 10 BG155663 | BG155663 saa64a06. |
| 14 | 281.2 | 14.3 | 700 | 10 BG587404 | BG587404 EST489176 |
| 15 | 277.2 | 14.1 | 686 | 10 BG452287 | BG452287 NF083C09L |
| 16 | 272 | 13.8 | 626 | 9 AI728708 | AI728708 BNLGH114 |
| 17 | 271.2 | 13.8 | 438 | 9 AI993756 | AI993756 701497447 |

| | | | | | |
|----|-------|------|-----|-------------|--------------------|
| 18 | 264 | 13.4 | 578 | 10 BM177413 | BM177413 saj81a10. |
| 19 | 263.8 | 13.4 | 716 | 12 BH483575 | BH483575 BOHQX86TR |
| 20 | 257.4 | 13.1 | 671 | 10 BG443698 | BG443698 GA_Ea002 |
| 21 | 255.8 | 13.0 | 450 | 9 AW396192 | AW396192 sh02e12.y |
| 22 | 255 | 13.0 | 494 | 10 BG510374 | BG510374 sac76h08. |
| 23 | 249.8 | 12.7 | 636 | 12 BH456518 | BH456518 BOGRX42TR |
| 24 | 245.4 | 12.5 | 511 | 10 BG790472 | BG790472 sae58a03. |
| 25 | 242.4 | 12.3 | 531 | 10 BG467356 | BG467356 00978 lea |
| 26 | 237.8 | 12.1 | 525 | 10 BF003363 | BF003363 EST431861 |
| 27 | 236.6 | 12.0 | 524 | 10 BE329503 | BE329503 so66b12.y |
| 28 | 235.2 | 12.0 | 408 | 9 AV423888 | AV423888 AV423888 |
| 29 | 230 | 11.7 | 430 | 9 AV413998 | AV413998 AV413998 |
| 30 | 228.8 | 11.6 | 501 | 10 BM358370 | BM358370 GA_Ea000 |
| 31 | 227.8 | 11.6 | 494 | 10 BI972280 | BI972280 sag99e03. |
| 32 | 226.6 | 11.5 | 610 | 9 AW585919 | AW585919 EST317542 |
| C | 223 | 11.4 | 714 | 9 AW348855 | AW348855 GM210010A |
| 34 | 219 | 11.2 | 563 | 10 BG043071 | BG043071 st91h01.y |
| 35 | 218.8 | 11.1 | 563 | 10 BF588097 | BF588097 FMI_37_F0 |
| 36 | 218.4 | 11.1 | 452 | 9 AI416823 | AI416823 sal8006.y |
| 37 | 214.2 | 10.9 | 666 | 12 BG2460 | BG2460 T21N16TF TA |
| 38 | 211 | 10.7 | 436 | 10 BF324736 | BF324736 sul4g09.y |
| 39 | 209.8 | 10.7 | 473 | 9 AW734476 | AW734476 sk94h05.y |
| 40 | 208 | 10.6 | 626 | 10 BF009011 | BF009011 ss72c03.y |
| 41 | 200.6 | 10.2 | 846 | 12 BG2171 | BG2171 T20L13TF TA |
| 42 | 195.2 | 9.9 | 708 | 10 BG586497 | BG586497 EST488265 |
| 43 | 194.2 | 9.9 | 465 | 9 AL378474 | AL378474 MEBB38D11 |
| C | 193 | 9.8 | 427 | 9 AW310145 | AW310145 sf31q08.x |
| 45 | 191 | 9.7 | 321 | 10 T46205 | T46205 9468 Lambda |

ALIGNMENTS

RESULT 1

BE204113

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. .626

/organism="Medicago truncatula"

/cultivar="genotype A17"

/db_xref="taxon:3880"

/clone="PKV0-14D23"

/clone_lib="KV0"

/tissue_type="Seedling roots"

626 bp mRNA linear EST 05-SEP-2000
KV0 Medicago truncatula cdna clone PKV0-14D23, mRNA

sequence.

BE204113

BE204113.1 GI:8747396

EST

barrel medic.

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;

Medicago.

1 (bases 1 to 626)

VandenBosch,K., Endre,G., Hur,J., Moore,J., Beremand,P., Ellis,L.,

Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and

Fraser,C.M.

ESTs from uninoculated seedling roots of Medicago truncatula

Unpublished (1999)

Contact: VandenBosch K

Department of Biology

Texas A&M University

College Station, TX 77843-3258, USA

Tel: 409 845 7707

Fax: 409 845 2891

Email: kate@mail.bio.tamu.edu

Texas A&M University name:T263885e

TIGR sequence name:MTGA0247K

More information is available at.

http://chrysis.tamu.edu/medicago

Seq primer: SKmod (CTA gaa CTA gtg gat CC).

LOCUS BI270025 563 bp mRNA linear EST 18-JUL-2001
 DEFINITION NF003D04FL1042 Developing flower Medicago truncatula cDNA clone
 ACCESSION BI270025
 VERSION BI270025.1 GI:14877244
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.
 REFERENCE 1 (bases 1 to 563)
 AUTHORS Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
 Flores, H.R., Iman, J.T., Weller, J.W. and May, G.D.
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 JOURNAL Medicago truncatula flower library
 COMMENT Unpublished (2001)
 CONTACT: May GD
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7391
 Fax: 580 221 7380
 Email: gdmay@noble.org
 Insert Length: 563 Std Error: 0.00
 Plate: 003 row: D column: 04
 Seq primer: TCACACAGGAACAGCTATGAC.
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 source Location/Qualifiers
 1..563
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="NF003D04FL"
 /clone_lib="Developing flower"
 /tissue_type="Developing flowers"
 /dev_stage="Developmentally pooled. Contains a mixture of
 very young, developing, fully-opened flowers and flowers
 in early transition into pods."
 /notes="Vector: Lambda Zap; cDNA was prepared from polyA+
 enriched, pooled samples of equivalent amounts of total
 RNA from very young, developing, fully-opened flowers and
 flowers transitioning into pods. The cDNA was
 directionally ligated into the Uni-Zap XR vector
 (Stratagene) and packaged using the Gigapack III Gold
 packaging extracts. Phagemids containing cDNA inserts were
 in vivo excised from the recombinant Uni-Zap XR vector
 using Exassist helper phage and the E. coli strain
 XLI-Blue MRF' (Stratagene). Excised plasmids were plated
 using SOUR cells."
 BASE COUNT 139 a 116 c 127 g 177 t 4 others
 ORIGIN
 Query Match 17.4%; Score 342.6; DB 10; Length 563;
 Best Local Similarity 76.1%; Pred. No: 2.5e-69;
 Matches 439; Conservative 0; Mismatches 123; Indels 15; Gaps 1;
 Qy 751 ggagaattcgtactgcgcgaagctcgttggaagcaaatcgattctctagctgttctca 810
 Db 1 GAATTAATCAAGATGCGGAGGCTTGGTTAAACACATCGGATACGTAGCTGTATCACA 60
 Qy 811 aatcgagctatgagaaagtcgcttactctcgcgaagctctcgcgcgcgagattta 870
 Db 61 AGAAGGCTCTATGAGAAAGTTGCAACCTATTTCGCTGAAGTTTGTAGTAGAAGAACTA 120
 Qy 871 ccgtctctccgtcgcagagtcgaatcccaatcgaccactctctctccgatactcttcagatgca 930
 Db 121 CGGTGTGTTTCC-----ACAGCATTCGGTTTCCGATTCACATTCAGTTCAGATCCA 165
 Qy 931 cttctagagagattgtcttatctcaagttcgtcacttcacgcgcgaatcaagcattct 990
 Db 166 TTTCTATGAAACTGTCTTAATAAATTCGCTACCTTCGATTCGGAATCAAGCTATTCT 225

Qy 991 cgaagctttcaagggaagaaagagttcatgttcattgtattctctatgatgagtcgaaggtc 1050
 Db 226 AGAAGCTTTTCAAGGAAATCTAGTGTTCATGTGATTTCTCGATTTAATCAAGGAT 285
 Qy 1051 tcaatggcgcgccttatgcaggctcttgcgcttcgacctgggtggctcctctgtttccg 1110
 Db 286 CGAGTGGCGCGCTTATGAGGACCTTGTTCACGTCCTGGGGTCTCTCTGCTTTTCG 345
 Qy 1111 gttaacgcggaattggtccaccgcgcgcgataatttcgattatctctcatgaagtgggtg 1170
 Db 346 GTTGACCGGAATCGGACCTCGGCGTGGATAACTCAGATCACTTCAACAAGTGGGTG 405
 Qy 1171 taagctggctcattagctgagcgattcactggttgagttgagtagacagagattgtg9c 1230
 Db 406 GAGCTTGCCTCAATTTCACAAAACGATTTCATGTTTTCAGTTTGTAGTATCGTGTGTTGTC 465
 Qy 1231 taacatttagctgattctgattctgctgattcagctgagcttagaccagagtagattgaatc 1290
 Db 466 TAATAGTTTACGCTGATCTTGATGCTTCGATGCTTGAATCGGNCACCGGAACGGAATC 525
 Qy 1291 tgttgcggttaactctgttttcgagcttcacaagctc 1327
 Db 526 TGTTCGGNTAACTCTGNTTTTGANCTTCATAAACTC 562
 RESULT 4
 234599/c
 LOCUS ATTS3359 Versailles-VB Arabidopsis thaliana cDNA clone VBVD10,
 DEFINITION mRNA sequence.
 ACCESSION 234599
 VERSION 234599.1 GI:506916
 KEYWORDS EST.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 REFERENCE 1 (bases 1 to 372)
 AUTHORS CNRS.
 TITLE The Arabidopsis thaliana transcribed genome: the GDR cDNA program
 JOURNAL Unpublished (1996)
 COMMENT Contact: Desprez T., Anselem J., Chiapello H., Rouze P., Caboche
 M., Hofte H.
 INRA Versailles
 Laboratoire de Biologie Cellulaire
 Route de Saint-Cyr, 78026 Versailles Cedex, France
 Email: thierryversailles.inra.fr.
 FEATURES
 source Location/Qualifiers
 1..372
 /organism="Arabidopsis thaliana"
 /strain="ecotype Columbia"
 /db_xref="taxon:3702"
 /clone="VBVD10"
 /clone_lib="Versailles-VB"
 /tissue_type="whole seedlings"
 /dev_stage="in vitro-grown etiolated seedlings, 5 days old"
 /note="Vector: pBluescript"
 BASE COUNT 113 a 97 c 73 g 88 t 1 others
 ORIGIN
 Query Match 17.0%; Score 333.4; DB 10; Length 372;
 Best Local Similarity 98.9%; Pred. No: 3.4e-67;
 Matches 356; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
 Qy 1587 agcgtcatgaaacgttg-agtcagtgaggaacacgggttcgggtctgctgggttcgagct 1645
 Db 359 ACCGTCATGAACCGTTGAAGTCANTGGAGAACCGGTTCCGGGTCTGCTGGGTTTCGGCT 300
 Qy 1646 gcatattgttcgaatgcgtttaagcaagcgaatgcttttggctctgttcaacggc 1705
 Db 299 GCACATATTGGTTCGATGCCGTTTAAGCAAGCGAGTAGTCTTTGGCTCTCTGTTCAACGGC 240


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FEATURES
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    1. .743
      /organism="Medicago truncatula"
      /cultivar="genotype A17"
      /db_xref="taxon:3880"
      /clone="PKV3-22R24"
      /clone_lib="KV3"
      /tissue_type="Seedling roots"
      /dev_stage="3 days post-inoculation with Sinorhizobium
      meliloti"
      /lab_host="E. coli strain XLOLR"
      /note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
      XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
      was directionally ligated into the Unizap XR vector from
      Stratagene and packaged using Gigapack III Gold packaging
      extracts. Plasmids containing cDNA inserts were excised
      from the recombinant lambda-zap phage using Ex-assist
      helper phage and propagated in XLOLR cells."
    193 a 170 c 165 g 215 t

```

| | | | | | | | | | |
|----|------|--|--------|--------------|--------|------------|------|--------|------|
| | | Query Match | 15.4%; | Score | 302.2; | DB | 9; | Length | 743; |
| | | Best Local Similarity | 68.3%; | Pred. | No. | 6.6e-60; | | | |
| | | Matches | 453; | Conservative | 0; | Mismatches | 198; | Indels | 12; |
| | | Gaps | | | | | | | |
| Qy | 833 | gctacttacttcgcgaagctctcgcgcggcgattaccgtctctctccctgcagagt | 892 | | | | | | |
| Db | 1 | GCTTCCATTTTCGCACRAGCACTTGCAAGAAGAACTCAGCGTAAC-----CCAGAAGAA | 54 | | | | | | |
| Qy | 893 | ccaatcgacacctctctctcgcatactctcgaattcactctcgaatgcactctcgaagacttgctcttat | 952 | | | | | | |
| Db | 55 | ACAATCGATTTCATCTCTCAGAAAATCTTCCACATGCACTTCTTAGAATCTTCACCTTAT | 114 | | | | | | |
| Qy | 953 | ctcaagttcgtcacttcacgcgcgaatacaacgcgattctcgaagctttttccaagggaagaaa | 1012 | | | | | | |
| Db | 115 | CTCAAATTCGGCTCATTTTCACGTCTAATCAACTATCTCGAAGCTTTCGCCGGTGC CGGA | 174 | | | | | | |
| Qy | 1013 | agagttcatgtcattgatattctctatgatgcgaaggtcttcaatggcgcggcgcttatgcag | 1072 | | | | | | |
| Db | 175 | AGAGTTCATGTTATAGATTTTGGTCTTAAACAAGGGATGCAATGGCCTGCGCTTATGCAA | 234 | | | | | | |
| Qy | 1073 | gctcttgcgcttcgaacctggtggtctctctgttttcocggttaaacgcgaatatgggtccaccg | 1132 | | | | | | |
| Db | 235 | CGCGTGGCATTTACGTCCTTCGGCGGTCCTCTACGTTCCGGTTTAAACGGCATCGCACCGCG | 294 | | | | | | |
| Qy | 1133 | gcacgcgaataattcgcattatcttcataagaattggttgttaagctgggtccatttagctgag | 1192 | | | | | | |
| Db | 295 | CAGCGGACAAATACGTATGCTTTTGCACACAAAGTTGGCTGSAATTAAGCTCAGCTGCTCAG | 354 | | | | | | |
| Qy | 1193 | gcgattcacgttggttagtacagagatttggtgcatacaacttagctgatcttgat | 1252 | | | | | | |
| Db | 355 | ACAAATCGGTGTTTCAGTTCCGAATTTTCGTGGATTTGTTGTTGAACAGATATTTCGGGATCTTGAC | 414 | | | | | | |
| Qy | 1253 | gcttcgatctgttagcttagaccaagttagattgaatctgttgcggtttaactcgttttc | 1312 | | | | | | |
| Db | 415 | CCGAATAATGCTTGAGATCCGACC GCG-----TGAAGCTGTTCGCTGTTAACTCCGTTTTTC | 468 | | | | | | |
| Qy | 1313 | gagcttcacaagctcttgggacacactggtgcgatacgataaggtcttggtggtgagat | 1372 | | | | | | |
| Db | 469 | GAGCTTCATACCATGTTAGCTTCGACCCCGGTTTCAGTTGAGAAAGTTCTCAACACATGTTAAG | 528 | | | | | | |
| Qy | 1373 | cagattaacccggagattttcactgtggttagcaggaatcgaaaccataatagtcagatt | 1432 | | | | | | |
| Db | 529 | AAGATAAACCTTAAATCGTAACTCTGTGAGAAAGGCAATCAATCAACGACCGGTT | 588 | | | | | | |

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QY 1433 ticttagatcggtttactgagtcgttgatctattactgacgcttctgtgactcggttgaa 1492
Db 589 TCTGAGACGGGTTTACCGAAGCTTTACATTATTACTCAAGCTTATTCTGACTTGGAG 648
QY 1493 ggt 1495
Db 649 GGT 651

RESULT 8
LOCUS 234183
DEFINITION ATTS3217 Versailles-VB Arabidopsis thaliana cDNA clone VBVD10,
mRNA sequence.
ACCESSION 234183
VERSION 234183.1 GI:498540
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 343)
CNRS.
The Arabidopsis thaliana transcribed genome: the GDR cDNA program
Unpublished (1996)
Contact: Desprez T., Anselme J., Chiapello H., Rouze P., Caboche
M., Hofte H.
INRA Versailles
Laboratoire de Biologie Cellulaire
Route de Saint-Cyr, 78026 Versailles Cedex, France
Email: thierry@versailles.inra.fr.
Location/Qualifiers
1. 343
/organism="Arabidopsis thaliana"
/strain="ecotype Columbia"
/db_xref="taxon:3702"
/clone="VBVD10"
/clone_lib="Versailles-VB"
/tissue_type="whole seedlings"
/dev_stage="in vitro-grown etiolated seedlings, 5 days old"
/note="vector: phuescript"
BASE COUNT 86 a 79 c 92 g 85 t 1 others
ORIGIN

Query Match 15.2%; Score 298; DB 10; Length 343;
Best Local Similarity 97.1%; Pred. No. 6e-59;
Matches 335; Conservative 0; Mismatches 6; Indels 4; Gaps 3;

QY 500 gagtacatcttaagctattcccggtgagcggtattctcaatcagttcgctatcgattcg 559
Db 1 GAGTACGATCTTAAGCTATTCCCGGTGACGCGATTCTCAATCACTGTCGATCGATTTCG 60
QY 560 gcttcttcgttaaccaggcggtgaggagatcgctatactacaacaaagggttgaaa 619
Db 61 GCTTCTTCGTTACCAAGCGCGGAGGAGATACGTATCTACAAACACGCGTTGAAA 120
QY 620 tgcctaacggcgctggtggaacaccacacgacgagctgag-tcaactcggcattgtt 678
Db 121 TGCTCAACGCGCGTGTGGAACACCATACACGACGCGCTGAGATCAACTCGGCATGTGT 180
QY 679 cctggttactcgaggaacggtgtcgctctcgttcacgcgcttttggcttgcgtg- 737
Db 181 CCTGGTTACTCGCAGGAGAACGGTGTGCGCTCTCGTTTCACGCGCTTTTGGCTGCGCTGA 240
QY 738 aagctgttcagaaggagaatctgactgtggtggaagctctggtgaagcaaatcgattct 797
Db 241 AAGCTGTTCAGAAAGACAATCTGACTCTAGCGGA--NTCTGGTGAGCAATCGGATTCT 298
QY 798 tagctgtttctcaaatcgagagctatgagaaaagtgcgtacttact 842
Db 299 TAGCCGTTTCTCAAAATCGGAGCATGAGAAAAGTCGCTACTTACT 343

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RESULT 9

AW704479

LOCUS

DEFINITION

AW704479.1

GI:7588689

EST.

KEYWORDS

SOURCE

ORGANISM

soybean.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Glycine.

1 (bases 1 to 579)

Shoemaker, R., Keim, P., Vodkin, L., Erpelidg, J., Corvelli, V., Khanna

A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,

Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers

Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk

R., Ritter, E., Kohn, S., Shin, T., Jackson, F., Cardenas, M., McCann

R., Waterston, R. and Willson, R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130

South Memorial Parkway Huntville, AL 35801 For further information

call: (800)-533-4363 or contact via email: ccu@resgen.com

Insert length: 1731 Std Error: 0.00

Seq primer: -40RP from Gibco

High quality sequence stop: 424.

Location/Qualifiers

1. 579

/organism="Glycine max"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-cl019-6311"

/clone_lib="Gm-cl019"

/tissue_type="Immature seed coats of greenhouse grown

plants"

/lab_host="DH10B (Gibco BRL)"

/note="Vector: pSPORT1 (Life Technologies); Site_1: Not I;

Site_2: Sal I; This cDNA library was constructed from mRNA

isolated from Immature seed coats (200-300 mgs) of

greenhouse grown plants. The library was prepared using

the Life Technologies pSuperScript cDNA library

construction kit. Complementary DNA was synthesized from

mRNA using a poly (dT) sequence with a Not I restriction

site. Sal I linker adapters were ligated to the

blunt-ended cDNA fragments followed by Not I digestion.

The cDNA fragments were directionally cloned into the Not

I-Sal I restriction site of the pSPORT1 vector. The

ligated cDNA fragments were transformed into E. coli

Electromax DH10B host cells (Gibco BRL). This library was

constructed by Dr. Liia Vodkin and Dr. Anu Khanna."

BASE COUNT 123 a 175 c 173 g 108 t

ORIGIN

Query Match 14.8%; Score 291.4; DB 9; Length 579;

Best Local Similarity 73.3%; Pred. No. 2.2e-57;

Matches 392; Conservative 0; Mismatches 131; Indels 12; Gaps 1;

QY 654 cggctgagtcacactcgcatgttgcctgctgactcgcagagagacggtgtgctgtcg 713

Db 56 CCGACGAGTCAAGCGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 115

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Qy 714 ttacgcgcgttttgcttgcgtgaagctgttcaagaagagaatctgactgtggcggaag 773
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 116 TGCACAGCCTCATGCGTGCAGGAGCGGTGGAGAACACAAACCTCGCCGTGGCGGAG 175

Qy 774 ctctggtgaagcaaatcggattcttagctgtttctcaaatcggagctatgagaaatcgc 833
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 176 CGCTGGTGAAGCAGATCGCGTCTCCGTGTGTGTCGACAGTTGGAGCTATGAGAAAGTCG 235

Qy 834 ctactacttcgcgaagctctcgcgcgcggaattaccgtctctctcctcgcgcagagtc 893
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 236 CAATCTACTTTCGCCGAACGCTCGGAGCGCAATCTACAGAGTCTTCCCTCTGC----- 289

Qy 894 caatgaccactctctctccatactcttcagatgcactctcagagactgttctcttacc 953
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Db 290 -----AACACTCTCTCTCCGATTCCTTCAGATTCACTTCTACGAAACCTGTCCATACC 343

Qy 954 tcaagtctgcactcctcgcgaatcgaagcattctcgaagcttttcaagggaagaaaaa 1013
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Qy 1014 gattcatgcatgattctctatgagtcgaaggtcttcaatgcccgcgccttatgcagg 1073
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Qy 1074 ctcttgcttcgactggtggtctctctctgttttccggttaaccggaattggtccaccgg 1133
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RESULT 10
BI498716 BI498716 579 bp mRNA linear EST 30-NOV-2001
LOCUS
DEFINITION sal2il1.y1 Gm-cl053 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl053-4101 5' similar to TR:023642 O23642 RGAI1 PROTEIN. [1]
; mRNA sequence.
ACCESSION BI498716
VERSION BI498716.1 GI:15338060
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 579)
AUTHORS Shoemaker,R., Kelm,P., Vodkin,L., Erpeliding,J., Coryell,V., Khanna
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
CONTACT: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 for further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 421.
FEATURES
Location/Qualifiers
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/db_xref="taxon:3847"
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grown"
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XhoI; The Harosoy NIL was constructed and seed was
provided by Dr. J. Specht, University of Nebraska
(Shoemaker and Specht, 1995). The cDNA library was
constructed from mRNA isolated from whole seedlings of 3
week old greenhouse grown plants. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site and a 3'
anchor. EcoRI adapters were ligated to the blunt-ended
cDNA fragments followed by XhoI digestion. The cDNA
fragments were directionally cloned into the EcoRI-XhoI
restriction site of the pBluescript vector. The ligated
cDNA fragments were transformed into DH10B host cells
(GibcoBRL). This library was constructed in cooperation
with Dr. Paul Kelm's laboratory at Northern Arizona
University."
BASE COUNT 119 a 174 c 171 g 115 t
ORIGIN
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Matches 413; Conservative 0; Mismatches 162; Indels 9; Gaps 2;
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Qy 1322 aagctcttggagacacctgtgtgcgataaggttcttgggtggtggaatcagattaaa 1381
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Qy 1382 ccgagattttcactgtggttgacaggaatcgaacataatagctccgattttcttagat 1441
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Db 535 GTGAACCCCTAAACGATAAGGCCATGTCGGAGGTTTACTTAGGAA 578

RESULT 11
BH52965/c BH52965 739 bp DNA linear GSS 14-DEC-2001
LOCUS
```


sp. glycines (Plant Cell Report 18:375-380). Cultivar PI 567374 is partially resistant to the disease SDS. Plant tissue (expanded leaves, folded leaves, and new shoots) were collected at 1, 6, 24, and 48 hrs. after inoculation and their mRNA pooled equally for cDNA construction. The library was prepared using the Stratagene pBluescript II SK(+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA insert is protected from XhoI digestion via methylation during first strand synthesis. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells. Plants were inoculated by Shuxian Li (Glen Hartman lab, University of Illinois). Library was constructed by Steve Clough (Lila Vodkin lab, University of Illinois)."

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| Qy | 926 | atgcactctacgagactgttccttatctcaagttcgtcacttcacgcggaatcaagcg 985 | | |
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| Qy | 1046 | ggtctcaatggcgcgcttatcgagctcttcgctctgcactgagctgggtcctctctgt 1105 | | |
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| LOCUS | BG155663 | 543 bp | mRNA | linear |
| DEFINITION | saa64a06.y1 Gm-cl01060 Glycine max cDNA clone GENOME SYSTEMS CLONE | EST 28-NOV-2001 | | |
| | ID: Gm-cl01060-1188 5', similar to TR:023642 023642 RGAI PROTEIN. [1] | | | |

| | | | | | |
|-----------------------|--|--|-----------------|-------------|---------|
| ACCESSION | BG155663 | | | | |
| VERSION | BG155663.1 | GI:12689327 | | | |
| KEYWORDS | EST. | | | | |
| SOURCE | soybean. | | | | |
| ORGANISM | Glycine max | | | | |
| REFERENCE | 1 (bases 1 to 543) | | | | |
| AUTHORS | Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. | | | | |
| TITLE | Public Soybean EST Project | | | | |
| JOURNAL | Unpublished (1999) | | | | |
| COMMENT | Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com High quality sequence stop: 419. | | | | |
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| | /lab_host="DH10B" | | | | |
| | /note="vector: pbluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from root tissue of 2 week old seedlings for PI468916. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pbluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed in the laboratory of Dr. Randy Shoemaker at Iowa state university." | | | | |
| BASE COUNT | 112 a | 169 c | 155 g | 107 t | |
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| Db | 2 | CTTACTTAAAGTTCCGCGCACTTCACCGCAACACGCGGATTCGGAAGCGTTTCAGGGA | 61 | | |
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| Db | 122 | TGCAAGCCCTTGCGCTTCGCAACGAGCGGCCCTCCCGCTTTCCGGCTTAACCGGAATCGGAC | 181 | | |
| QY | 1128 | caccggcaccgataatttcgattatcttcataagttggtgtaagctggctcatttag | 1187 | | |
| Db | 182 | CGCCGGCGGCGGACAACTCCGACCACTCCAGGAGGTAGGTTGGAAGCTCGCGCAGCTGG | 241 | | |

| | | | |
|------------|------|--|------|
| Qy | 1188 | ctgaggcgatcaacgcttgagttggtacagaggattgtggtcaacacttttagctgac | 1247 |
| Db | 242 | CGGAGAGGATCCACGTGCAGTTCGAGTACCGCGGCTTCGTCGAACAGCCTCGCGGATC | 301 |
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| Qy | 1308 | tttcgagcttcacaagctctcttggacgacacctggtcgatcgataagattcttgggtg | 1367 |
| Db | 356 | TCTTCGAGTTTCACAAGCTCTCGCCCCCGCGCGGTGAGAAAGTCTCTCCGTCG | 415 |
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| Db | 476 | TGAGTTGTTCGACGGGATCCAGGAGTCACTGCACTATTATTCAACTCTATTTCAGACTGC | 535 |
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| ORGANISM | | | |
| REFERENCE | | | |
| AUTHORS | | | |
| TITLE | | | |
| JOURNAL | | | |
| COMMENT | | | |
| FEATURES | | | |
| source | | | |

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